AMENDMENTS TO THE DRAWINGS

Please replace drawing Figures 1-8, filed February 18, 2005, with the enclosed replacement Figures 1-8.

REMARKS

Claims 20, 21, and 38-56 are pending in this application. Claims 1-19, 22-37, and 57 have been canceled. Claims 20, 21, 38-41, and 56 are withdrawn from consideration, as directed to non-elected inventions, in response to the Restriction Requirement mailed June 16, 2008.

Independent claim 42 has been amended to correct a typographical error by replacing "on" with "one" (reciting "at least one transposon insertion..."). The word "site" has been inserted after two occurrences of "transposon insertion." Claim 42 now also recites for clarity that "polynucleotide sequences of transposon insertion sites" (rather than "transposon insertions") are collected and mapped. See, for example, page 25 line 14 to page 26, line 12, referring to the collection of polynucleotide sequence information of the transposon insertion sites in biochemical or electronic form. Claim 42 has also been amended to define the abbreviation HTTIM as High Throughput Transposon Insertion Map and to clarify that the polynucleotide sequences of transposon insertion sites form an HTTIM database. See, for example, page 10, lines 15-18. Dependent claims 45 and 46 have been amended to recite that the HTTIM database comprises the polynucleotide sequences of at least about 3,000 to 6,000, or about 4,000 to 5,000, transposon insertion sites, respectively. See page 10, lines 6-9.

Claim 42 has also been amended to replace "the genomic sequence of the bacterium" and "genomic sequence database" with "the Staphylococcus genome," as recited earlier in this claim, and dependent claim 43 has been amended to recite that the Staphylococcus genome is an *S. aureus* genone. See, for example, page 8, lines 9-10. Claim 52 has been amended to recite a statistical calculation that utilizes a Bayessian statistical model. See page 49, lines 10-13.

The claim amendments add no new matter.

Sequence Rules Compliance

The specification has been amended to insert or correct the sequence identifiers after the sequences on pages 42, 43, and 45 of the specification. Sequence identifiers have also been inserted on page 15, in reference to the sequences shown in Figures 6-8. All sequences were included in the paper copy and computer readable form of the Sequence Listing submitted February 18, 2005.

Please withdraw the sequence objections.

Drawings

A set of formal replacement drawings, having a better image quality than the originally filed drawings, accompanies this response.

Please withdraw the drawing objections.

Specification

Trademarks

Page 48 of the specification has been amended to identify GENBANK® as a registered trademark, as noted on page 3 of the Office Action. Applicant has reviewed and amended the specification to additionally clarify that MF59™, TWEEN®, SPAN®, and PLURONIC™ are trademarks. Generic terminology has been included where not apparent from the specification.

Embedded Hyperlinks

Pages 15 and 46 of the specification have been amended to remove the embedded hyperlinks and refer instead to Internet domain and path names.

Please withdraw the specification objections.

Rejections under 35 U.S.C. § 112, ¶ 2

Claims 42-55 have been rejected as indefinite for the reasons on pages 4 and 5 of the Office Action. As noted above, amended claim 42 now correctly recites "at least one [instead of "on"] transposon insertion," providing antecedent basis for "said at least one transposon insertion." Claim 42 has also been amended to clarify that "polynucleotide sequences of transposon insertion sites" (rather than "transposon insertions") are collected and mapped.

Claim 43 has been amended to recite that the Staphylococcus genome is an *S. aureus* genone. Claims 45 and 46 have been amended to recite that the High Throughput Transposon Insertion Map (HTTIM) database comprises polynucleotide sequences of at least about 3,000 to 6,000, or about 4,000 to 5,000, transposon insertion sites, respectively. Finally, claim 52 has been amended to recite a statistical calculation that utilizes a Bayessian statistical model.

Please withdraw the rejections under 35 U.S.C. § 112, ¶2.

Rejection under 35 U.S.C. § 103(a)

Claims 42-55 have been rejected as obvious under 35 U.S.C. § 103(a) over the combination of Charles *et al.* (WO 01/07651; "Charles") and Haselbeck *et al.* (WO 01/70955; "Haselbeck"). Applicants respectfully traverse.

Claim 42 and its dependent claims 43, 44, and 47-55 are all directed to a method for identifying a library of putative essential or important genes using a High Throughput Transposon Insertion (HTTIM) database. The method comprises (a) mutagenizing a *Staphylococcus* genome with a transposon such that individual cells having at least one transposon insertion site are isolated and (b) collecting and mapping polynucleotide sequences of the transposon insertion sites in each individual cell to form a database of the polynucleotide sequences of transposon insertion sites (HTTIM database). The method further comprises (c)

comparing the database of transposon insertion sites with a database comprising the *Staphylococcus* genome to identify open reading frames that are not disrupted by a transposon insertion and (d) forming a library from the putative or important genes that are not disrupted by a transposon.

Claims 45 and 46 depend from claim 42 and further recite that the HTTIM database, used to identify the library of putative essential or important genes, comprises polynucleotide sequences of at least about 3,000 to about 6,000, or at least about 4,000 to 5,000, transposon insertion sites.

It is black letter law that obviousness requires at least a suggestion of all of the features in a claim. See *CFMT, Inc. v. Yieldup Intern. Corp.*, 349 F.3d 1333, 1342 (Fed. Cir. 2003). The combination of Charles and Haselbeck fails to meet this legal standard, at least because neither reference suggests the feature of "collecting and mapping polynucleotide sequences of said at least one transposon insertion site...so as to form a database of said polynucleotide sequences of transposon insertion sites," as claimed.

Nowhere does the primary reference Charles suggest sequencing transposon insertion sites in order to form a database of polynucleotide sequences, according to the claimed invention. Haselbeck similarly fails to suggest forming a database of transposon insertion polynucleotide sequences. Haselbeck does not mention transposon insertion at all. In contrast to the disclosures of the cited references, Applicants alone teach the mapping of gene or gene fragment sequences containing transposon insertion sites, and comparing a database of these polynucleotide sequences (numbering, for example, from 3,000 to 8,000) to the bacterial genome in order to form a library of putative essential or important genes. See, for example, the procedures on page 46, line 20 to page 50, line 2 of the specification.

Since the combination of Charles and Haselbeck does not suggest all of the claimed features, *prima facie* obviousness is not established. Please withdraw the rejection under 35 U.S.C. § 103(a).

CONCLUSION

In view of the above amendments remarks, all pending claims of this application are believed to be in condition for allowance. Acknowledgement of the same is respectfully requested. This response is believed to completely address all of the substantive issues raised in the Office Action dated December 19, 2008.

Respectfully submitted,

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Date: June 19, 2009

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